

## SEQUENCE LISTING

<110> Meyers, Rachel  
Hunter, John Joseph

<120> 62112, A NOVEL HUMAN DEHYDROGENASE AND  
USES THEREOF

<130> MNI-187

<150> 60/229,831

<151> 2000-08-31

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1932)

<400> 1

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      Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
        1             5             10

cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
  15             20             25             30

cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
             35             40             45

aaa atc aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat 252
Lys Ile Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
             50             55             60

gaa ctt aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc 300
Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe
             65             70             75

act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
             80             85             90

gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
             95             100             105             110

gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
             115             120             125

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"FASTA" format

aga cta ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg 492  
 Arg Leu Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu  
 130 135 140

gca gcg cac cag gct att ggc ctc aag ggg atc atc ttg gct ggc act 540  
 Ala Ala His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr  
 145 150 155

gag gag cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac 588  
 Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His  
 160 165 170

att gca gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc 636  
 Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala  
 175 180 185 190

tca atc cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc 684  
 Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile  
 195 200 205

ctc aat ggc tcc aag gtc tgg att act aat gga gga ctg gcc aat att 732  
 Leu Asn Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile  
 210 215 220

ttt act gtg ttt gca aag act gag gtc gtt gat tct gat gga tca gtg 780  
 Phe Thr Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val  
 225 230 235

aaa gac aaa atc aca gca ttc ata gta gaa aga gac ttt ggt gga gtc 828  
 Lys Asp Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val  
 240 245 250

act aat ggg aaa ccc gaa gat aaa tta ggc att cgg ggc tcc aac act 876  
 Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr  
 255 260 265 270

tgt gaa gtc cat ttt gaa aac acc aag ata cct gtg gaa aac atc ctt 924  
 Cys Glu Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu  
 275 280 285

gga gag gtc gga gat ggg ttt aag gtg gcc atg aac atc ctc aac agc 972  
 Gly Glu Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser  
 290 295 300

ggc cgg ttc agc atg ggc agc gtc gtg gct ggg ctg ctc aag aga ttg 1020  
 Gly Arg Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu  
 305 310 315

att gaa atg act gct gag tac gcc tgc aca agg aaa cag ttt aac aag 1068  
 Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys  
 320 325 330

agg ctc agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct 1116  
 Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala  
 335 340 345 350

cag aag gct tac gtc atg gag agt atg acc tac ctc aca gca ggg atg 1164  
 Gln Lys Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met  
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09945326-033101

[illegible]

610

615

620

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tgcacctgaa ggggtgtcgc ctggcctggg agagcctctt ccagggtttg acctgcaggc 2112
agtgtctctt aacaggacca tcacagcttc tgaactgagc cggagagaga gaatggaatt 2172
gctgaccctt ggaactggcg ggtattctgg tcattgagga gacaccatag tggaaactgg 2232
ggcttatgct gctgcctcca ggggtgtgagg tgggtgggga cctgtgtcag gtgtggatag 2292
ccatttctgc tcaaccacac attctctaag aaacagcttg aaagctctgt ctgggtcatt 2352
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<212> PRT

<213> Homo sapiens

<400> 2

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Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
 35          40          45
Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
 50          55          60
Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
 65          70          75          80
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
 85          90          95
Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
100          105          110
Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
115          120          125
Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
130          135          140
His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
145          150          155          160
Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
165          170          175
Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
180          185          190
Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
195          200          205
Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
210          215          220
Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
225          230          235          240
Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
245          250          255
Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
260          265          270
Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
275          280          285
Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
290          295          300
Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
305          310          315          320
Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
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030301

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<221> CDS  
<222> (1) ... (1863)
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1				5				10						15		
tgc	cgg	ggt	ctg	gtg	gtc	tct	acc	gcg	aac	cgg	cgg	cta	ctg	cgc	acc	96
Cys	Arg	Gly	Leu	Val	Val	Ser	Thr	Ala	Asn	Arg	Arg	Leu	Leu	Arg	Thr	
			20				25						30			
agc	ccg	cct	gta	cga	gct	ttc	gcc	aaa	gag	ctt	ttc	cta	ggc	aaa	atc	144
Ser	Pro	Pro	Val	Arg	Ala	Phe	Ala	Lys	Glu	Leu	Phe	Leu	Gly	Lys	Ile	
			35				40						45			
aag	aag	aaa	gaa	gtt	ttc	cca	ttt	cca	gaa	gtt	agc	caa	gat	gaa	ctt	192
Lys	Lys	Lys	Glu	Val	Phe	Pro	Phe	Pro	Glu	Val	Ser	Gln	Asp	Glu	Leu	

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aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc act gaa			240
Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu			
65	70	75	80
gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca gat gaa			288
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu			
	85	90	95
act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa gtc cca			336
Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro			
	100	105	110
gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca aga cta			384
Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu			
	115	120	125
ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg gca gcg			432
Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala			
	130	135	140
cac cag gct att ggc ctc aag ggg atc atc ttg gct ggc act gag gag			480
His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu			
	145	150	155
cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac att gca			528
Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala			
	165	170	175
gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc tca atc			576
Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile			
	180	185	190
cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc ctc aat			624
Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn			
	195	200	205
ggc tcc aag gtc tgg att act aat gga gga ctg gcc aat att ttt act			672
Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr			
	210	215	220
gtg ttt gca aag act gag gtc gtt gat tct gat gga tca gtg aaa gac			720
Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp			
	225	230	235
aaa atc aca gca ttc ata gta gaa aga gac ttt ggt gga gtc act aat			768
Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn			
	245	250	255
ggg aaa ccc gaa gat aaa tta ggc att cgg ggc tcc aac act tgt gaa			816
Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu			
	260	265	270
gtc cat ttt gaa aac acc aag ata cct gtg gaa aac atc ctt gga gag			864
Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu			
	275	280	285
gtc gga gat ggg ttt aag gtg gcc atg aac atc ctc aac agc ggc cgg			912
Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg			
	290	295	300

09945326-083101

ttc agc atg ggc agc gtc gtg gct ggg ctg ctc aag aga ttg att gaa 960  
 Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu  
 305 310 315 320

atg act gct gag tac gcc tgc aca agg aaa cag ttt aac aag agg ctc 1008  
 Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu  
 325 330 335

agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct cag aag 1056  
 Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys  
 340 345 350

gct tac gtc atg gag agt atg acc tac ctc aca gca ggg atg ctg gac 1104  
 Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met Leu Asp  
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caa cct ggc ttt ccc gac tgc tcc atc gag gca gcc atg gtg aag gtg 1152  
 Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val  
 370 375 380

ttc agc tcc gag gcc gcc tgg cag tgt gtg agt gag gcg ctg cag atc 1200  
 Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu Gln Ile  
 385 390 395 400

ctc ggg ggc ttg ggc tac aca agg gac tat ccg tac gag cgc ata ctg 1248  
 Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg Ile Leu  
 405 410 415

cgt gac acc cgc atc ctc ctc atc ttc gag gga acc aat gag att ctc 1296  
 Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu Ile Leu  
 420 425 430

cgg atg tac atc gcc ctg acg ggt ctg cag cat gcc ggc cgc atc ctg 1344  
 Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg Ile Leu  
 435 440 445

act acc agg atc cat gag ctt aaa cag gcc aaa gtg agc aca gtc atg 1392  
 Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr Val Met  
 450 455 460

gat acc gtt ggc cgg agg ctt cgg gac tcc ctg ggc cga act gtg gac 1440  
 Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr Val Asp  
 465 470 475 480

ctg ggg ctg aca ggc aac cat gga gtt gtg cac ccc agt ctt gcg gac 1488  
 Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu Ala Asp  
 485 490 495

agt gcc aac aag ttt gag gag aac acc tac tgc ttc ggc cgg acc gtg 1536  
 Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg Thr Val  
 500 505 510

gag aca ctg ctg ctc cgc ttt ggc aag acc atc atg gag gag cag ctg 1584  
 Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu Gln Leu  
 515 520 525

gta ctg aag cgg gtg gcc aac atc ctc atc aac ctg tat ggc atg acg 1632  
 Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly Met Thr  
 530 535 540

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Ala	Val	Leu	Ser	Arg	Ala	Ser	Arg	Ser	Ile	Arg	Ile	Gly	Leu	Arg	Asn	
545					550					555					560	
cac	gac	cac	gag	gtt	ctc	ttg	gcc	aac	acc	ttc	tgc	gtg	gaa	gct	tac	1728
His	Asp	His	Glu	Val	Leu	Leu	Ala	Asn	Thr	Phe	Cys	Val	Glu	Ala	Tyr	
				565					570						575	
ttg	cag	aat	ctc	ttc	agc	ctc	tct	cag	ctg	gac	aag	tat	gct	cca	gaa	1776
Leu	Gln	Asn	Leu	Phe	Ser	Leu	Ser	Gln	Leu	Asp	Lys	Tyr	Ala	Pro	Glu	
			580					585					590			
aac	cta	gat	gag	cag	att	aag	aaa	gtg	tcc	cag	cag	atc	ctt	gag	aag	1824
Asn	Leu	Asp	Glu	Gln	Ile	Lys	Lys	Val	Ser	Gln	Gln	Ile	Leu	Glu	Lys	
		595					600					605				
cga	gcc	tat	atc	tgt	gcc	cac	cct	ctg	gac	agg	aca	tgc				1863
Arg	Ala	Tyr	Ile	Cys	Ala	His	Pro	Leu	Asp	Arg	Thr	Cys				
	610					615						620				

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